variants have about 90% identity to the human protein as shown in the table below. The first column shows the SEQ ID_H for the human cDNA; the second column, the SEQ ID_{VAR} for variant cDNAs; the third column, the clone numbers for the variants; the fourth column, the percent identity to the human cDNA; and the fifth column, the nucleotide alignment (Nt_H) of the human and variant cDNAs.

SEQ ID_H	SEQ ID_{VAR}	Clone No.	Identity	Nt_H Alignment
1	9	702758636	89%	541-1123
1	10	034237_Mm.1	90%	667-1173
1	11	702482342	89%	671-1173

C1

IN THE CLAIMS

Please amend claims 24, 26, 27, 31, 32, and 34 as follows.

For the Examiner's convenience, all pending claims are listed below. Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "Version with markings to show changes made."

24. (Once Amended) An isolated polypeptide selected from the group consisting of:

C2

a) a polypeptide comprising an amino acid sequence of SEQ ID NO:1,

b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1, and

c) an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1.

25. An isolated polypeptide of claim 24 comprising an amino acid sequence of SEQ ID NO:1.

26. (Once Amended) An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

C3

a) a polypeptide comprising an amino acid sequence of SEQ ID NO:1,

b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1, and

c) an immunogenic fragment of a polypeptide consisting of an amino acid sequence of SEQ ID NO:1.

C3

27. (Once Amended) An isolated polynucleotide encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:1.

28. An isolated polynucleotide of claim 27 comprising a polynucleotide sequence of SEQ ID NO:2.

29. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 26.

30. A cell transformed with a recombinant polynucleotide of claim 29.

31. (Once Amended) A method of producing a polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence of SEQ ID NO:1,

b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1, and

C4

c) an immunogenic fragment of a polypeptide consisting of an amino acid sequence of SEQ ID NO:1,

the method comprising:

1) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide of claim 26, and

2) recovering the polypeptide so expressed.

C4

32. (Once Amended) A method of claim 31, wherein the polypeptide comprises an amino acid sequence of SEQ ID NO:1.

33. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence of SEQ ID NO:2,

b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence of SEQ ID NO:2,

c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

C5

34. (Once Amended) An isolated polynucleotide consisting of 60 contiguous nucleotides of a polynucleotide of claim 33.

35. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 33, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

36. A method of claim 35, wherein the probe comprises at least 60 contiguous nucleotides.

37. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 33, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

38. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 27, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

39. A method of assessing toxicity of a test compound, the method comprising:

a) treating a biological sample containing nucleic acids with the test compound,

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 33 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 33 or fragment thereof,

c) quantifying the amount of hybridization complex, and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.